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P2

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N. WOODSON
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PATENT APPLICATION SERIAL NO. _____

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PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53 (c).

Express Mail Label No. *EV336616999US*

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)
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☐ *Additional inventors are being named on the _____ separately numbered sheets attached hereto*

TITLE OF THE INVENTION (500 characters max)

METHOD AND SYSTEM FOR DETERMINATION OF MOLECULAR INTERACTION PARAMETERS

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OR

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Country		Telephone		Fax	

ENCLOSED APPLICATION PARTS (check all that apply)

☒ Specification *Number of Pages*   **31**   ☐ CD(s), Number _____

☒ Drawing(s) *Number of Sheets*   **8**   ☒ Other (specify)   **Fee Transmittal Form (+ copy)**

☒ Application Data Sheet. See 37 CFR 1.76

METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT

☐ Applicant claims small entity status. See 37 CFR 1.27.

☒ A check or money order is enclosed to cover the filing fees.

☐ The Director is hereby authorized to charge filing
fees or credit overpayments to Deposit Account Number: **19-1090**

☐ Payment by credit card. Form PTO-2038 is attached.

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The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☒ No.

☐ Yes, the name of the U.S. Government agency and the Government contract number are: _____.

Respectfully submitted,			
SIGNATURE		DATE 12/1/03	December 1, 2003
TYPED or PRINTED NAME	**Karl R. Hermanns**	REGISTRATION NO. (if appropriate)	33,507
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USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT

FEE TRANSMITTAL
for FY 2004

Patent fees are subject to annual revision.

Application Number	
Filing Date	**December 1, 2003**
First Named Inventor	**R bert Karlsson**
Examiner Name	
Art Unit	

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TOTAL AMOUNT OF PAYMENT	($)	160.00

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METHOD OF PAYMENT

☒ Payment Enclosed:

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Deposit Account Number	19-1090
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FEE CALCULATION

1. BASIC FILING FEE

Large Entity Fee Code	Fee($)	Small Entity Fee Code	Fee($)	Fee Description	Fee Paid
1001	770	2001	385	Utility filing fee	
1002	340	2002	170	Design filing fee	
1003	530	2003	265	Plant filing fee	
1004	770	2004	385	Reissue filing fee	
1005	160	2005	80	Provisional filing fee	160

SUBTOTAL (1)   ($) 160

2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE

	Extra Claims	Fee from below	Fee Paid
Total Claims			
Independent Claims			
Multiple Dependent			

Large Entity Fee Code	Fee ($)	Small Entity Fee Code	Fee ($)	Fee Description
1202	18	2202	9	Claims in excess of 20
1201	86	2201	43	Independent claims in excess of 3
1203	290	2203	145	Multiple dependent claim, if not paid
1204	86	2204	43	** Reissue independent claims over original patent
1205	18	2205	9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2)   ($)

**or number previously paid, if greater; For Reissues, see above

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FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Fee Code	Fee ($)	Small Fee Code	Fee ($)	Fee Description	Fee Paid
1051	130	2051	65	Surcharge - late filing fee or oath	
1052	50	2052	25	Surcharge - late provisional filing fee or cover sheet.	
1053	130	1053	130	Non-English specification	
1812	2520	1812	2520	For filing a request for *ex parte* reexamination	
1804	920*	1804	920*	Requesting publication of SIR prior to Examiner action	
1805	1840*	1805	1840*	Requesting publication of SIR after Examiner action	
1251	110	2251	55	Extension for reply within first month	
1252	420	2252	210	Extension for reply within second month	
1253	950	2253	475	Extension for reply within third month	
1254	1480	2254	740	Extension for reply within fourth month	
1255	2010	2255	1005	Extension for reply within fifth month .	
1401	330	2401	165	Notice of Appeal	
1402	330	2402	165	Filing a brief in support of an appeal	
1403	290	2403	145	Request for oral hearing	
1451	1510	1451	1510	Petition to institute a public use proceeding	
1452	110	2452	55	Petition to revive – unavoidable	
1453	1330	2453	665	Petition to revive – unintentional	
1501	1330	2501	665	Utility issue fee (or reissue)	
1502	480	2502	240	Design issue fee	
1503	640	2503	320	Plant issue fee	
1460	130	1460	130	Petitions to the Commissioner	
1807	50	1807	50	Processing fee under 37 CFR 1.17(q)	
1806	180	1806	180	Submission of Information Disclosure Stmt	
8021	40	8021	40	Recording each patent assignment per property (times number of properties)	
1809	770	2809	385	Filing a submission after final rejection (37 CFR § 1.129(a))	
1810	770	2810	385	For each additional invention to be examined (37 CFR § 1.129(b))	
1801	770	2801	385	Request for Continued Examination (RCE)	
1802	900	1802	900	Request for expedited examination of a design application	

Other fee (specify) _____

*Reduced by Basic Filing Fee Paid   SUBTOTAL (3)   ($)

SUBMITTED BY

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Signature		Date	December 1, 2003	00500

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APPLICATION DATA SHEET

Application Information

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Number of copies of CDs::

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                                            DETERMINATION OF MOLECULAR
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1   Initial   12/1/03

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Representative Information

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METHOD AND SYSTEM FOR DETERMINATION OF MOLECULAR INTERACTION PARAMETERS

5 ## BACKGROUND OF THE INVENTION

Field of the invention

The present invention relates to the determination of kinetic parameters for molecular interactions, and more particularly to a method for determining kinetic parameters for the interaction between a molecule immobilised to a solid

10 support surface and a binding partner to the molecule in solution. The invention also relates to an analytical system, a computer program product and a computer system for performing the method.

Description of the related art

15 Analytical sensor systems that can monitor interactions between molecules, such as biomolecules, in real time are gaining increasing interest. These sensor systems, usually referred to as interaction analysis sensor systems or biospecific interaction analysis sensor systems, are often based on optical biosensors and affinity analysis and offer a rapid way to determine in

20 real time *inter alia* equilibrium and rate constants without the need to label the interacting molecules. They have been used in the study of a variety of biomolecules, including proteins, nucleic acids, lipids and carbohydrates. In these systems, a sensor surface having one of the molecular reactants immobilised thereto is contacted with a solution containing the other reactant,

25 either by providing a flow of the solution past the sensor surface, or in a cuvette or the like, and binding interactions at the surface are detected.

Conventionally, to determine, for example, association and dissociation rate constants (k_a and k_d, respectively) for the interaction between two interacting molecules, one of the molecules, often referred to as the ligand, is

30 immobilised to a sensor surface and the other molecule, often referred to as the analyte, is provided in solution at several different known concentrations. Each concentration, or sample, of the analyte is then contacted with the sensor

surface, either in a laminar flow past the sensor surface or in a cuvette or the like to permit association of the analyte to the sensor surface. After a sample has been brought to contact the sensor surface, the surface is contacted with a solution free from analyte, usually buffer, to permit dissociation of the analyte

5   from the immobilised ligand. During these association and dissociation phases, the amount of binding of analyte to the surface is continuously detected and the binding data is collected. Before contacting the sensor surface with sample of a new analyte concentration, the ligand surface is restored or "regenerated" by treating the surface with a regeneration solution capable of removing any bound

10   analyte while not destroying the ligand. In that way, all the different samples will contact essentially one and the same ligand surface as far as ligand density is concerned. The association and dissociation rate constants can then be obtained from the collected binding data by fitting the data to mathematical descriptions of interaction models in the form of differential equations. Usually,

15   the binding data for all the samples are used in the same fit, a procedure referred to as global fitting. From the determined association and dissociation rate constants k_a and k_d, the equilibrium constant, K_D, and the affinity constant K_A ($K_A=1/K_D$) of the interaction can in turn be calculated. Alternatively, provided that the interaction reaches steady state during the association phase,

20   the equilibrium constant can be directly obtained from the binding data without fitting.

Problems may arise, however, when the ligands are covalently immobilised to the sensor surface and suitable regeneration conditions are difficult to find. Renewed binding of the ligand via an immobilised capture agent

25   before the contacting with each new analyte concentration could then be an alternative, but has the disadvantage of consuming large amounts of ligand for the determination.

Determination of equilibrium constants by a titration procedure without the requirement for regeneration of the immobilised ligands is described by

30   Schuck, P., et al. (1998) *Anal. Biochem.* **265**, 79-91. The sample is continuously circulated in a closed loop over two sensor spots of a commercial surface plasmon resonance biosensor. One of the sensor spots is functionalized with an

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immobilised ligand for a soluble analyte in the sample, and the other sensor spot serves as a reference surface. A binding isotherm for the interacting molecules is obtained by stepwise equilibrium titration of the analyte into the circulating loop, i.e. the sensor spots are sequentially contacted with stepwise increased concentrations of analyte until equilibrium is attained for each concentration. This equilibrium titration is said to be especially useful for the determination of binding constants in high-affinity systems since it eliminates the need for interpretation of binding kinetics and thereby problems that may arise from mass transport limitations.

A similar stepwise equilibrium titration procedure is described for a cuvette-based biosensor design in Hall, D. R., and Winzor, D. J. (1997) *Anal. Biochem.* **244**, 152-160.

Also Myszka, D. G., et al. (1998) *Anal. Biochem.* **265**, 326-330 discloses equilibrium analysis of high affinity interactions using a surface plasmon resonance-based biosensor. In this approach, the time available to collect association phase data is increased by placing the analyte directly into the running buffer. Complete equilibrium binding profiles were generated without a regeneration step by changing the concentration of analyte and allowing the surface reactions to reequilibrate. Analyte concentrations were also decreased to demonstrate that the binding reactions were fully reversible. In this way, equilibrium dissociation constants for very high affinity interactions could be determined.

Shank-Retzlaff, M. L., and Sligar, S. G. (2000) *Anal. Chem.* **72**, 4212-4220 describes a one-step method for determining kinetic rates and equilibrium binding affinities by a technique called analyte-gradient surface plasmon resonance SPR (AG-SPR) which eliminates the need for surface regeneration. A gradient of analyte is passed over the sensor surface under continuous-flow conditions so that the concentration of analyte increases linearly with time. The rate at which analyte binds to immobilised ligands on the sensor surface is monitored by monitoring the change in the surface plasmon resonance as the analyte concentration increases. Kinetic rates are determined by fitting the data

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to a two-compartment model for the molecular interaction which permits use also for systems under mass transport limitations.

Titration procedures to determine binding capacity and regeneration conditions have been proposed by Karlsson, R., et al., Biasymposium 1998, Edinburgh 2-4 September 1998, 5th Biasymposium in Japan, Tokyo, November 5-6, 1998.

US-A1-2003/014365 discloses a method for determining interaction parameters, including rate constants, between an analyte and a ligand immobilised to a sensor surface, where a measurement can be performed several times in succession, e.g. in a cuvette, with a stepwise modification of the analyte concentration each time. The measurements need not be completed to equilibrium but can be interrupted earlier and the concentration of the analyte can be raised or lowered. Separate fitting of the binding curve part corresponding to each analyte concentration is used to determine respective initial binding rates, from which the association and dissociation rate constants for the interaction are then determined.

.Thus, while titration procedures in combination with biosensors and affinity analysis are known *per se* in the art for determining equilibrium binding affinities, the use of multiple titrations to determine kinetic rate constants seems to be disclosed only in the above-mentioned publications Shank-Retzlaff, M. L., and Sligar, S. G. (2000), and US-A1-2003/014365. The method according to Shank-Retzlaff, M. L., and Sligar, S. G. suffers from the limitation that it requires the use of a continuous gradient of the analyte. The method of US-A1-2003/014365, on the other hand, is disadvantageous in that initial binding rates are frequently lower than the kinetic binding rate due to transport limitations, making initial binding rates unreliable for kinetic analysis. Further, this type of evaluation restricts the injection order of analyte concentrations.

From the prior art it may therefore be concluded that for determining kinetic rates for molecular interactions using systems based on biosensors and affinity analysis, it is necessary to regenerate the immobilised ligand prior to contacting the sensor surface with a different concentration of analyte to thereby present essentially one and the same ligand surface to each analyte

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concentration, unless (i) a continuous gradient of the analyte is used, or (ii) initial binding rates are determined in systems free from mass transport limitations.

It is an object of the present invention to provide a sensor-based method for determining chemical interaction parameters, including kinetic rate constants, by stepwise titration, which method obviates regeneration procedures while permitting measurements under mass transport limitation.

BRIEF SUMMARY OF THE INVENTION

According to the present invention, it has surprisingly been found that the above and other objects and advantages can achieved by an affinity sensor-based method for determining chemical interaction parameters, which method comprises performing, in one and the same experimental cycle, stepwise changes of the analyte concentration without intermediate regeneration of the sensor surface, and determining the interaction parameters using global analysis of the whole set of detected binding data with regard to a kinetic model for the molecular interaction that allows for mass transport limitation, such as e.g. the afore-mentioned two-compartment model. In this method, kinetic data can thus be obtained in spite of mass transport limitations and the different analyte concentrations may be used in any order.

Therefore, in one aspect, the present invention provides a method of determining kinetic parameters for a reversible molecular interaction between a ligand immobilised to a sensor surface and a binding partner to the ligand in solution, comprising the steps of:

a) sequentially, without intermediate regeneration or renewal of the immobilised ligand, flowing a plurality of fluid volumes containing different known concentrations of the binding partner over the solid support surface to permit association of binding partner to the immobilised ligand,

b) flowing over the solid support surface a fluid volume free from binding partner to permit dissociation of binding partner from the ligand,

c) monitoring during steps a) and b) the momentary amount of binding partner bound to the solid support surface related to time and solution concentration of binding partner and collecting the binding data, and

d) determining the kinetic parameters by globally fitting a predetermined kinetic model for the interaction between the binding partner and the immobilised ligand to the collected binding data, which model allows for mass transport limitation at the solid support surface.

The solid support surface is preferably a sensor surface, i.e. one which produces a detectable signal in response to a binding interaction at the surface.

The term "monitoring" as used herein means that detection is performed at at least a plurality of times during steps a) and b), preferably at a large number of times.

In another aspect, the present invention provides a method for determining the concentrations of binding partner in a plurality of binding partner-containing samples.

In still another aspect, the present invention provides a method for determining kinetic parameters for a plurality of different binding partners.

In another aspect, the present invention provides an analytical system for studying molecular interactions, which system comprises data processing means for performing at least one of the methods.

In yet another aspect, the present invention provides a computer program comprising program code means for performing at least one of the methods.

In still another aspect, the present invention provides a computer program product comprising program code means stored on a computer readable medium or carried on an electrical or optical signal for performing at least one of the methods.

In another aspect, the present invention provides a computer system containing a computer program comprising program code means for performing at least one of the methods.

Other advantages, novel features and objects of the invention will become apparent from the following detailed description of the invention when considered in conjunction with the accompanying drawings.

5   BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a schematic side view of a biosensor system based on surface plasmon resonance (SPR).

Figure 2 is a representative sensorgram with a binding curve having association and dissociation phases.

10   Figure 3 is a representative sensorgram obtained by sequential injections of a kinase inhibitor (staurosporin) over a surface with immobilised kinase according to the method of the present invention.

Figure 4 is the sensorgram of Figure 3 having overlaid thereon the binding curve resulting from global fitting.

15   Figure 5 is an overlay plot of observed and fitted binding data for sequential injections of a carbonic anhydrase inhibitor (acetazolemide) over a surface with immobilised carbonic anhydrase.

Figure 6 is a similar overlay plot to that of Figure 5 for sequential injections of another carbonic anhydrase inhibitor (azosulfamide).

20   Figure 7 is a similar overlay plot to those of Figures 5 and 6 for sequential injections of still another carbonic anhydrase inhibitor (benzenesulfonamide).

Figure 8 is an overlay plot of observed and fitted binding data for sequential injections of a thrombin inhibitor (melagatran) over a surface with

25   immobilised thrombin.

Figure 9 is an overlay plot of four binding curves and fitted data, three curves (to the left) representing sensorgrams with single injections of analyte, and one curve (to the right) representing a sensorgram for sequential injections of analyte.

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DETAILED DESCRIPTION OF THE INVENTION

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by a person skilled in the art related to this invention. Also, the singular forms "a", "an", and "the" are meant to include plural reference unless it is stated otherwise.

As mentioned above, the present invention relates to the determination of molecular interaction parameters, including kinetic rate constants, for the interaction between a molecule immobilised to a solid support surface and a binding partner to the molecule in solution by a novel titration type method, preferably in combination with sensor based technology to study the molecular interactions and present the results in real time, as the interactions progress. Before describing the present invention in more detail, however, the general context in which the invention is used will be described.

Chemical sensors or biosensors are typically based on label-free techniques, detecting a change in a property of a sensor surface, such as e.g. mass, refractive index, or thickness for the immobilised layer, but there are also sensors relying on some kind of labelling. Typical sensor detection techniques include, but are not limited to, mass detection methods, such as piezoelectric, optical, thermo-optical and surface acoustic wave (SAW) device methods, and electrochemical methods, such as potentiometric, conductometric, amperometric and capacitance/impedance methods. With regard to optical detection methods, representative methods include those that detect mass surface concentration, such as reflection-optical methods, including both external and internal reflection methods, angle, wavelength, polarization, or phase resolved, for example evanescent wave ellipsometry and evanescent wave spectroscopy (EWS, or Internal Reflection Spectroscopy), both may include evanescent field enhancement via surface plasmon resonance (SPR), Brewster angle refractometry, critical angle refractometry, frustrated total reflection (FTR), scattered total internal reflection (STIR) – which may include scatter enhancing labels, optical wave guide sensors; external reflection imaging, evanescent wave-based imaging such as critical angle resolved imaging, Brewster angle resolved imaging, SPR-angle resolved imaging, and

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the like. Further, photometric and imaging/microscopy methods, "per se" or combined with reflection methods, based on for example surface enhanced Raman spectroscopy (SERS), surface enhanced resonance Raman spectroscopy (SERRS), evanescent wave fluorescence (TIRF) and

5 phosphorescence may be mentioned, as well as waveguide interferometers, waveguide leaking mode spectroscopy, reflective interference spectroscopy (RIfS), transmission interferometry, holographic spectroscopy, and atomic force microscopy (AFR).

Commercially available biosensors include the BIACORE® system

10 instruments, manufactured and marketed by Biacore AB, Uppsala, Sweden, which are based on surface plasmon resonance (SPR) and permit monitoring of surface binding interactions in real time between a bound ligand and an analyte of interest.

While in the detailed description and Examples that follow, the present

15 invention is illustrated in the context of SPR spectroscopy, and more particularly the BIACORE® system, it is to be understood that the present invention is not limited to this detection method. Rather, any affinity-based detection method where an analyte binds to a ligand immobilised on a sensing surface may be employed, provided that a change at the sensing surface can be measured

20 which is quantitatively indicative of binding of the analyte to the immobilised ligand thereon.

The phenomenon of SPR is well known, suffice it to say that SPR arises when light is reflected under certain conditions at the interface between two media of different refractive indices, and the interface is coated by a metal film,

25 typically silver or gold. In the BIACORE® instruments, the media are the sample and the glass of a sensor chip which is contacted with the sample by a microfluidic flow system. The metal film is a thin layer of gold on the chip surface. SPR causes a reduction in the intensity of the reflected light at a specific angle of reflection. This angle of minimum reflected light intensity varies

30 with the refractive index close to the surface on the side opposite from the reflected light, in the BIACORE® system the sample side.

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A schematic illustration of the BIACORE® system is shown in Fig. 1. Sensor chip 1 has a gold film 2 supporting capturing molecules 3, e.g. antibodies, exposed to a sample flow with analytes 4 (e.g. an antigen) through a flow channel 5. Monochromatic p-polarised light 6 from a light source 7 (LED) is

5   coupled by a prism 8 to the glass/metal interface 9 where the light is totally reflected. The intensity of the reflected light beam 10 is detected by an optical detection unit (photodetector array) 11.

A detailed discussion of the technical aspects of the BIACORE® instrument and the phenomenon of SPR may be found in U.S. Patent No.

10   5,313,264. More detailed information on matrix coatings for biosensor sensing surfaces is given in, for example, U.S. Patent Nos. 5,242,828 and 5,436,161. In addition, a detailed discussion of the technical aspects of the biosensor chips used in connection with the BIACORE® instrument may be found in U.S. Patent No. 5,492,840. The full disclosures of the above-mentioned U.S. patents are

15   incorporated by reference herein.

When molecules in the sample bind to the capturing molecules on the sensor chip surface, the concentration, and therefore the refractive index at the surface changes and an SPR response is detected. Plotting the response against time during the course of an interaction will provide a quantitative

20   measure of the progress of the interaction. Such a plot is usually called a sensorgram. In the BIACORE® system, the SPR response values are expressed in resonance units (RU). One RU represents a change of 0.0001° in the angle of minimum reflected light intensity, which for most proteins and other biomolecules correspond to a change in concentration of about 1 pg/mm^2 on

25   the sensor surface. As sample containing an analyte contacts the sensor surface, the ligand bound to the sensor surface interacts with the analyte in a step referred to as "association." This step is indicated on the sensorgram by an increase in RU as the sample is initially brought into contact with the sensor surface. Conversely, "dissociation" normally occurs when the sample flow is

30   replaced by, for example, a buffer flow. This step is indicated on the sensorgram by a drop in RU over time as analyte dissociates from the surface-bound ligand.

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A representative sensorgram (binding curve) for a reversible interaction at the sensor chip surface is presented in Fig. 2, the sensing surface having an immobilised capturing molecule, or ligand, for example an antibody, interacting with a binding partner therefor, or analyte, in a sample. (The detection curves,

5 or sensorgrams, produced by biosensor systems based on other detection principles mentioned above will have a similar appearance.) The y-axis indicates the response (here in resonance units, RU) and the x-axis indicates the time (here in seconds). Initially, buffer is passed over the sensing surface giving the baseline response A in the sensorgram. During sample injection, an

10 increase in signal is observed due to binding of the analyte. This part B of the binding curve is usually referred to as the "association phase". Eventually, a steady state condition is reached where the resonance signal plateaus at C (this state may, however, not always be achieved). At the end of sample injection, the sample is replaced with a continuous flow of buffer and a decrease in signal

15 reflects the dissociation, or release, of analyte from the surface. This part D of the binding curve is usually referred to as the "dissociation phase". The analysis is ended by a regeneration step where a solution capable of removing bound analyte from the surface, while (ideally) maintaining the activity of the ligand, is injected over the sensor surface. This is indicated in part E of the sensorgram.

20 Injection of buffer restores the baseline A and the surface is now ready for a new analysis.

From the profiles of the association and dissociation phases B and D, repectively, information regarding the binding and dissociation kinetics is obtained, and the height of the resonance signal represents surface

25 concentration (*i.e.*, the response resulting from an interaction is related to the change in mass concentration on the surface). This will now be explained in more detail below.

Assume a reversible reaction between an analyte A and a surface-bound (immobilised) capturing molecule, or ligand, B which is not diffusion or mass

30 transfer limited and obeys pseudo first order kinetics:

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$$A + B \Leftrightarrow AB$$

This interaction model (usually referred to as the Langmuir model), which assumes that the analyte (A) is both monovalent and homogenous, that the ligand (B) is homogenous, and that all binding events are independent, is in fact applicable in the vast majority of cases.

The rate of change in surface concentration of analyte A (= rate of change in concentration of formed complex AB) during analyte injection is the sum of the rates of the analyte A going on and off:

$$\frac{d[AB]}{dt} = k_a[A][B] - k_d[AB] \qquad (1)$$

where [A] is the concentration of analyte A, [B] is the concentration of the ligand B, [AB] is the concentration of the reaction complex AB, k_a is the association rate constant, and k_d is the dissociation rate constant.

After a time t, the concentration of unbound ligand B at the surface is $[B_T] - [AB]$, where $[B_T]$ is the total, or maximum, concentration of ligand B. Insertion into Equation (1) gives:

$$\frac{d[AB]}{dt} = k_a[A]\{[B_T] - [AB]\} - k_d[AB] \qquad (2)$$

In terms of detector response units (AB is detected), this can be expressed as

$$\frac{dR}{dt} = k_a C(R_{max} - R) - k_d R \qquad (3)$$

where R is the response at time t in resonance units (RU), C is the initial, or bulk, concentration of free analyte (A) in solution, and R_{max} is the response (in RU) obtained if analyte (A) had bound to all ligand (B) on the surface. Rearrangement of Equation (3) gives:

$$\frac{dR}{dt} = k_a C R_{max} - (k_a C + k_d)R \qquad (4)$$

where R is the response in resonance units (RU). In integrated form, the equation is:

$$R = \frac{k_a C R_{max}}{k_a C + k_d}\left(1 - e^{-(k_a C + k_d)t}\right) \qquad (5)$$

Now, according to equation (4), if dR/dt is plotted against the bound analyte concentration R, the slope is $k_aC + k_d$ and the vertical intercept is $k_aR_{max}C$. If the bulk concentration C is known and R_{max} has been determined (e.g. by saturating the surface with a large excess of analyte), the association

5   rate constant k_a and the dissociation rate constant k_d can be calculated. A more convenient method is, however, fitting of the integrated function (5), or numerical calculation and fitting of the differential Equation (4), preferably by means of a computer program as will be described below.

The rate of dissociation can be expressed as:

10
$$\frac{dR}{dt} = -k_d R \qquad (6)$$

and in integrated form:

$$R = R_0 \cdot e^{-k_d t} \qquad (7)$$

where R_0 is the response at the beginning of the dissociation phase (when the buffer wash of the surface starts).

15   Equation (6) may be linearized:

$$\ln\left[\frac{R}{R_0}\right] = -k_d t \qquad (8)$$

and a plot of $\ln[R/R_0]$ versus t will produce a straight line with the slope = $-k_d$. More conveniently, however, the dissociation rate constant k_d is determined by fitting the exponential rate equation (7).

20   Affinity is expressed by the association constant $K_A = k_a/k_d$, or the dissociation constant (also referred to as the equilibrium constant) $K_D = k_d/k_a$.

The association constant K_A may alternatively be determined from Equation (3), where dR/dt = 0 at equilibrium, giving:

$$k_d R_{eq} = k_a C (R_{max} - R_{eq}) \qquad (9)$$

25   where R_{eq} is the detector response at equilibrium. Since $k_a/k_d = K_A$, insertion in Equation (9) and rearrangement gives:

$$\frac{R_{eq}}{C} = -K_A R_{eq} + K_A R_{max} \qquad (10)$$

If binding reactions are performed at multiple concentrations, the data may either be fitted or R_{eq}/C may be plotted versus R_{eq} which gives the slope

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= -K_A. Such an equilibrium analysis may be performed when the rates of association and dissociation are too rapid to measure accurately.

To obtain reliable kinetic constants, the above described analysis is usually repeated for a number of different analyte concentrations and, suitably, also at at least one other ligand density at the sensor surface.

Software for the analysis of kinetic and other biosensor data is commercially available. Thus, for example, evaluation of kinetic data produced by the BIACORE® instruments is usually performed with the dedicated BIAevaluation software (supplied by Biacore AB, Uppsala, Sweden) using numerical integration to calculate the differential rate equations and non-linear regression to fit the kinetic parameters by finding values for the variables that give the closest fit reducing the sum of squared residuals to a minimum. The residuals are the difference between the calculated and the experimental curve at each point, squared residuals being used to weight equally deviations above and below the experimental curve. The sum of squared residual is expressed by Equation (11):

$$S = \sum_{1}^{n} (r_f - r_x)^2 \qquad (11)$$

where S is the sum of squared residuals, r_f is the fitted value at a given point, and r_x is the experimental value at the same point.

For example, for the molecular interaction described above, such software-assisted data analysis is performed by, after subtracting background noises, making an attempt to fit the above-mentioned simple 1:1 Langmuir binding model as expressed by Equations (5) and (7) above to the measurement data.

Usually the binding model is fitted simultaneously to multiple binding curves obtained with different analyte concentrations C (and/or with different levels of surface derivatization R_{max}). This is referred to as "global fitting", and based on the sensorgram data such global fitting establishes whether a single global k_a or k_d will provide a good fit to all the data. The results of the completed fit is presented to the operator graphically, displaying the fitted curves overlaid on the original sensorgram curves. The closeness of the fit is

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also presented by the chi-squared (χ^2) value, a standard statistical measure. For a good fitting, the chi-squared value is in the same magnitude as the noise in RU^2. Optionally, "residual plots" are also provided which give a graphical indication of how the experimental data deviate from the fitted curve showing

5   the difference between the experimental and fitted data for each curve. The operator then decides if the fit is good enough. If not, the sensorgram or sensorgrams exhibiting the poorest fit are excluded and the fitting procedure is run again with the reduced set of sensorgrams. This procedure is repeated until the fit is satisfactory.

10   -   Sometimes, the above-mentioned 1:1 binding reaction model will not be valid, which requires the data set to be reanalysed using one or more other reaction models. Such alternative models may include, for example, a one to one reaction influenced by mass transfer (mass transport), two parallel independent one to one reactions, two competing reactions, and a two state

15   reaction. Parallel reactions can occur when the immobilised ligand is heterogeneous, whereas a heterogenous analyte may give rise to competing reactions. A two state reaction indicates a conformation change that gradually leads to a more stable complex between ligand and analyte. For differential rate equations reflecting these alternative reaction models, it may be referred to, for

20   example, Karlsson, R., and Fält, A. (1997) J. Immunol. Methods 200, 121-133 (the disclosure of which is incorporated by reference herein). For a more comprehensive description of curve fitting with regard to the BIACORE® system, it may be referred to the BIAevaluation Software Handbook (Biacore AB, Uppsala, Sweden) (the disclosure of which is incorporated by reference

25   herein).

As regards mass transport, transport effects will influence the kinetics of binding when the reaction rate is fast compared to the rate of transport. For a reaction where analyte (A) binds to immobilised ligand (B), binding with mass transport limitation may be represented by the reaction formula:

30      $$A_{solution} \Leftrightarrow A_{surface} + B \Leftrightarrow AB$$

The differential equations describing the binding interaction will therefore include terms for mass transfer of analyte to the surface. For a flow cell, a "two-

compartment" model consisting of a set of coupled ordinary differential equations and described in *inter alia* Myszka, D. G., et al. (1998) *Biophys. J.* **75**, 583-594, and Shank-Retzlaff, M. L., and Sligar, S. G., supra (the relevant disclosures of which are incorporated by reference herein) is considered to give

5 a reasonable description of the binding kinetics when the data are influenced by mass transport. In this model, the flow cell is assumed to be divided into two compartments, one in which the concentration of analyte is constant; and a second near the sensor surface where the analyte concentration depends on the mass transport rate, the surface density of ligand, and the reaction rate

10 constants.

For the interaction of a monovalent analyte (A) reacting with an immobilised monovalent ligand (B), this model may be represented by the following two differential equations (12) and (13):

$$V_i \frac{dA}{dt} = S(-k_a A(B_T - AB) + k_d AB + k_t(C - A)) \quad (12)$$

15
$$\frac{dAB}{dt} = k_a A(B_T - AB) - k_d AB \quad (13)$$

where V_i is the volume of the inner compartment, S is the surface area of the flow chamber, k_t is the transport coefficient describing diffusive movement of analyte between the compartments, B_T is the total ligand concentration, A is the bulk concentration of free analyte, C is the injection (i.e. initial) analyte

20 concentration, AB is the concentration of complex AB (= surface density of bound analyte), and k_a and k_d are the association and dissociation rate constants, respectively.

It is understood that the use of this two-compartment model analyzing the kinetic globally will extend the range of reaction rates that can be

25 determined with instruments like the BIACORE® and has also been incorporated in the above-mentioned BIAevaluation analysis software (available from Biacore AB, Uppsala, Sweden).

Theoretical interaction data for different interaction models may be simulated using a simulator, such as e.g. the simulator which is built-in in the

30 above-mentioned BIAevaluation analysis software. In this way, the effects of varying experimental parameters may be explored, thereby helping to

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determine which interaction conditions that may be crucial in distinguishing between alternative kinetic models.

The invention

As mentioned above, determining kinetic parameters using, for example, a BIACORE® instrument, conventionally comprises monitoring the interaction of analyte with immobilised ligand for a plurality of different analyte concentrations with regeneration, or renewal, of the immobilised ligand before each measurement with a new analyte concentration. A kinetic model for the interaction is then fitted globally to the collected binding data, usually in the form of sensorgrams, to give the kinetic parameters.

According to the present invention, such a flow cell-based analysis for determining kinetic parameters may be substantially improved and speeded up by a titration type, or "sequential injection", procedure wherein the ligand-supporting surface is successively contacted, in one and the same analytical cycle, with the different analyte concentrations to produce a continuous sensorgram. A kinetic interaction model allowing for mass transport limitation, such as the two-compartment model mentioned above, is then fitted globally to the entire sensorgram to calculate the kinetic parameters. In addition to being considerably less time-consuming, this titration type method reduces the amount of experimental data to be evaluated and eliminates the risk of regeneration conditions destroying immobilised ligand.

The order of introducing the different analyte concentrations is not critical to the success of the inventive procedure. Rather, the analyte concentrations may, in fact, be introduced in any order. For example, the analyte concentrations may be successively increased, or successively decreased, or may alternately be higher and lower, etc. Further, the same concentration of analyte may be introduced repeatedly, if desired.

The injections of analyte, which preferably may be short, for a BIACORE® or similar instrument e.g. in the order of 30-60 seconds, may be interrupted when an increased analyte concentration only leads to a marginally increased response. This may advantageously be effected using so-called

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adaptive software. The formed complex is then preferably allowed to dissociate for a longer period of time, e.g. from about 5 to 60 minutes in the context of a BIACORE® or similar instrument, to add adequate dissociation data for the kinetic evaluation. Such a dissociation period may, optionally, instead (or

5   additionally) be performed between any two analyte injections in the cycle.

It is to be noted that the design of the above-mentioned BIACORE® instruments, for example, requires that each injection of analyte be followed by injection of running buffer, permitting partial dissociation of the bound analyte, before the next concentration of analyte is injected. It is understood that such

10   alternating analyte-free liquid volumes, for example with about one minute intervals, will add dissociation data to the those obtained by the above- · mentioned (preferably longer) dissociation period. Provided that sufficient dissociation data is obtained by these alternating injections of analyte–free fluid, the longer dissociation period may even be dispensed with. Intermediate buffer

15   injections may, of course, also be used, even if a sensor instrument design as · such permits sequential injections of analyte without buffer injections between them.

At least for some applications, it is preferred that the flow is substantially constant during the entire experimental cycle.

20   The sequential injection procedure may optionally be repeated at least once with the same or another sequence of analyte concentrations, and all the collected binding data may then be fitted simultaneously to the kinetic interaction model.

If desired, binding data from one or more sequential experiments

25   performed as as described above may be combined with binding data from one or more conventional type single concentration experiments, and the combined data are then fitted to the kinetic interaction model. Thus, generally, the total data set that is globally fitted to the kinetic interaction model may comprise any combination of binding curves including one or more "sequential" binding curves

30   and one or more single concentration binding curves.

To facilitate the understanding of the invention, reference is now made to Fig. 3 which shows an exemplary sensorgram (as obtained with the above-

mentioned BIACORE® instrument) for a titration with successively increased concentrations of an analyte (A) reacting with an immobilised ligand (B) to form a complex (AB) which gives rise to the detected SPR response. This titration is described in more detail in Example 1 below. Referring to the sensorgram,

5   analyte concentration 80 nM was injected between 404-464 seconds, 240 nM between 523-583 seconds, 730 nM between 642-702 seconds, and 2200 nM between 760-820 seconds. .

Before analysing the binding curve, start and end times for each injection of analyte is identified, and the base line is adjusted to zero level. Generally, the

10   binding curve may then be analysed using an interaction model based on time dependent analyte concentration and allowing for mass transport limitation, . such as the above-mentioned two-compartment model. If necessary, this model may be adapted to other interaction mechanisms, such as e.g. conformation change (A + B $\leftrightarrow$ AB $\leftrightarrow$ AB*), competing reactions (A1 +B $\leftrightarrow$ A1B; A2 + B $\leftrightarrow$

15   A2B), parallel reactions (A + B1 $\leftrightarrow$ AB1; A +B2 $\leftrightarrow$AB2), or bivalent analyte (A + B $\leftrightarrow$ AB; AB + B $\leftrightarrow$ AB2). Such models are described in more detail in, for example, the BIAevaluation Software Handbook mentioned above.

Assuming, for example, 1:1 binding, the following differential equation may represent the time dependent concentration of analyte A capable of

20   binding to immobilised ligand B.

$$\frac{dA}{dt} = k_t(C_1 + C_2 + C_3 + ...C_n - A) - (k_a A * B - k_d AB) \qquad (14)$$

where A is the surface concentration of free analyte A, k_t is a transport coefficient, C_1 to C_n are the different bulk concentrations of analyte, B is the concentration of immobilised ligand (ligand density), AB is the concentration of

25   formed complex (=bound analyte), and k_a and k_d are the association rate constant and dissociation rate constant, respectively.

If at the beginning of the experiment the analyte concentration, A, at the surface is assumed to be zero, the concentration of ligand, B, is assumed to be R_{max}, and the concentration of formed complex, AB, is assumed to be zero,

30   the following functions, here written in a form compatible with the above-mentioned BIAevaluation software, describe the interaction system.

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AB+RI1*$1+RI2*$2+RI3*$3+RI4*$4+RI5*$5;

$1=(sign(t-tOn1)-(sign(t-tOff1))/2;

$2=(sign(t-tOn2)-(sign(t-tOff2))/2;

$3=(sign(t-tOn3)-(sign(t-tOff3))/2;

$4=(sign(t-tOn4)-(sign(t-tOff4))/2;

$5=kt*($1*conc1+$2*conc2+$3*conc3+$4*conc4-A);

$6=ka*A*B-kd*AB;

A=$5-$6|0;

B=-$6|Rmax;

AB=$6|0

In the above model, sign functions $1 to $4 (being 1 or 0) indicate when a certain analyte concentration is injected (tOn1 is the time when analyte concentration 1 is injected, tOff1 is the time when analyte concentration 1 is stopped, etc). Functions $5 and $6 describe together the variation of the surface concentration of analyte over time, $6 describing how the ligand density and complex varies with time. The function on the first line corresponds to the total change in signal from binding AB and bulk effects present during each injection. By numerical integration of these equations and global fitting to all data points of the whole sensorgram in Fig. 3, using e.g. BIAevaluation software (Biacore AB, Uppsala, Sweden) adapted to the present invention, the kinetic rate constants k_a and k_d can be obtained. Mathematical models for the other interaction mechanisms may readily be devised by a person skilled in the art.

The result of the fit is shown in Fig. 4, where the solid "non-rippling line" indicates the adapted curve for best fit for the concentration range 80-2200 nM, k_a and k_d being constrained to single values of $1.0*10^5$ $M^{-1}s^{-1}$ and $6.6*10^{-4}$ s^{-1}, respectively, as described in Example 1 below.

With the above model, kinetic and affinity data can thus be obtained in spite of transport limitations. Since, as mentioned above, the method is insensitive to the injection order of analyte, analysis of relatively low analyte concentrations may be performed when binding is close to saturation or above the equilibrium response, thereby maximizing the kinetic information in the sensorgram where transport effects are small.

20

Data from binding analyses at two or more different ligand densitites may advantageously be fitted simultaneously.

Measurement of concentration simultaneously with kinetic rate constants may be performed, using the above titration procedure and data fitting, provided that the transport coefficient k_t is known and kept constant. Preferably, binding data from at least two, and preferably more ligand densities are then used.

A similar titration type approach as those above may also be used to determine (at least approximate) kinetic rate constants for a plurality of different analytes binding to the same ligand. In this case, different analytes are sequentially passed over the sensor surface rather than different analyte concentrations. The evaluation of the binding data is modified to permit fitting of different rate constants to the resulting total binding curve. Such a procedure may, for example, be used to screen different binding partners towards the ligand to quickly find the best binder, e.g. drug candidates binding to a drug target, such as a receptor. Optionally, this approach may be combined with the use of different analyte concentrations.

While it currently is preferred to use so-called label-free detection methods, including those mentioned above, such as SPR, other detection techniques may, as already mentioned above, of course, also be contemplated, such as those based on the detection of a label, e.g. a radiolabel, fluorophore (including surface fluorescence), chromophore, chemiluminescer, a marker for scattering light, an electrochemically active marker, a thermoactive marker, etc.

The methods of the invention, including titration (i.e. sequential analyte injections) and evaluation with time dependent analyte concentration, are, as already mentioned above, suitably reduced to practice in the form of a computer system running software which implements the different steps of the procedure. Preferably, the titration is adaptive as mentioned above. The invention also extends to computer programs, particularly computer programs on or in a carrier, adapted for putting the titration procedure of the invention into practice. The carrier may be any entity or device capable of carrying the program. For example, the carrier may comprise a storage medium, such as a ROM, a CD ROM or a semiconductor ROM, or a magnetic recording medium, for example a

floppy disc or a hard disk. The carrier may also be a transmissible carrier, such as an electrical or optical signal which may be conveyed via electrical or optical cable or by radio or other means. Alternatively, the carrier may be an integrated circuit in which the program is embedded.

5   Software like that outlined above may also be used to generate theoretical interaction curves for different interaction models similarly as described further above for the conventional single injection analysis procedures. By generating data for a complex model, for instance a conformation change model, varying parameters such as injection time and

10   analyte concentration and then fitting this data to both a 1:1 binding model and a conformational change model the residuals can identify conditions for optimal designs of kinetic experiments.

In the following Examples, various aspects of the present invention are disclosed more specifically for purposes of illustration and not limitation.

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EXAMPLES

Instrumentation

A BIACORE® S51 instrument (Biacore AB, Uppsala, Sweden) was used. This instrument has two Y-type flow cells which allow a dual flow of fluids over a

20   sensor chip surface, so-called hydrodynamic addressing, as described in, for example, EP-B1-1021703 (the disclosure of which is incorporated by reference herein). The instrument uses three parallel detection spots on the sensor chip. As sensor chip was used Series S Sensor Chip CM5 (Biacore AB, Uppsala, Sweden) which has a gold-coated surface with a covalently linked

25   carboxymethyl-modified dextran polymer hydrogel. The output from the instrument is a "sensorgram" which is a plot of detector response (measured in "resonance units", RU) as a function of time. An increase of 1000 RU corresponds to an increase of mass on the sensor surface of approximately 1 ng/mm^2.

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Example 1

Binding of a kinase inhibitor to immobilised kinase

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Anti-histidine antibody (Qiagen 34660; Qiagen, Venlo, Netherlands) was diluted to 20 □g/ml in 10 mM acetate buffer pH 5.0, and 13000 RU of antibody was immobilised to a Series S Sensor Chip CM5 using amine coupling according to the manufacturer's instructions. The flow was 10 µl/min. Histidine

5   tagged kinase (proprietary) was then captured and cross-linked to the sensor chip surface by injecting 30 □g/ml of the kinase in 10 mM PBS for three minutes followed by 2.5 min injections of EDC/NHS and ethanolamine to stabilise the kinase on the surface. With this procedure 4000 RU of kinase were immobilised.

10   A kinase inhibitor, staurosporin, was injected at concentrations of 80, 240, 730 and 2200 nM at a flow of 30 µl/min. The assay buffer was 50 mM Tris pH 7.5, 150 mM NaCl, 10 mM $MgCl_2$ and 3% DMSO. Overlay plots of observed and fitted data for the injection sequence are demonstrated in Figure 3 ·(observed) and Figure 4 (observed plus fitted). The association rate constant

15   was calculated to $1,0*10^5$ M^{-1} s^{-1}, and the dissociation rate constant k_d to $6,6*10^{-4}$ s^{-1}.

Example 2

Binding of a set of carbonic anhydrase inhibitors to immobilised carbonic

20   anhydrase

Carbonic anhydrase (Sigma C3640), 20 □g/ml in 10 mM acetate buffer pH 5.0, was immobilised to a Series S Sensor Chip CM5 using amine coupling according to the manufacturer's instructions, (flow 10 µl/min) to obtain sensor surfaces with approximately 2000 and 700 RU, respectively, of immobilised

25   carbonic anhydrase. Kinetic analysis was performed by injecting inhibitors in 10 mM PBS buffer with 0.005% P20 and 5% DMSO at a flow of 30 µl/min. The inhibitors were acetazoleamide (Sigma A6011), azosulfamide (Sigma A2759), and benzenesulfonamide (Aldrich 10,814-6), Overlay plots demonstrating observed and fitted data for the two ligand densities are presented in Figure 5

30   (acetazoleamide), Figure 6 (azosulfamide) and Figure 7 (benzenesulfonamide). In Figure 5, data represent two repeats on each ligand density, and k_a was calculated to $1,8*10^6$ M^{-1} s^{-1}, and k_d to $4,0*10^{-2}$ s^{-1}. In Figure 6, k_a was

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calculated to $2,9*10^4$ $M^{-1} s^{-1}$, and k_d to $8,1*10^{-3}$ s^{-1}, and in Figure 7 k_a was calculated to $1,6*10^5$ $M^{-1} s^{-1}$, and k_d to $1,4*10^{-1}$ s^{-1}.

Example 3

Binding of a high affinity inhibitor to immobilised thrombin

Thrombin (Sigma T 1063), 20 □g/ml in 10 mM acetate buffer pH 5.0, was immobilised to a Series S Sensor Chip CM5 using amine coupling according to the manufacturer's instructions (flow 10 µl/min), resulting in sensor surfaces with approximately 2300 and 600 RU, respectively, of immobilised thrombin. Kinetic analysis was performed by injecting a high affinity thrombin inhibitor, melagatran (a gift from Johanna Deinum, AstraZeneca, Mölndal, Sweden), in 10 mM PBS buffer with 0.005% P20, 5% DMSO and 3.4 mM EDTA at a flow of 30 µl/min. Overlay plots demonstrating observed and fitted data are presented in Figure 8. The calculated k_a was $2,0*10^7$ $M^{-1} s^{-1}$, and k_d $1,8*10^{-2}$ s^{-1}.

Examples 1 to 3 above demonstrate that a wide range of rate constants can be determined with the sequential injection procedure. In these Examples, k_a values range from $2,9*10^4$ to $2,0*10^7$ $M^{-1} s^{-1}$ and k_d values range from 0,14 to $6,6 \ 10^{-4}$ s^{-1}. The Examples also illustrate that kinetic data can be obtained using one or two ligand densities and that the injection order can be mixed and not only in the order from low to high concentration.

Example 4

Combined sequential and single injections

In Figure 9, simulated data representing sequential and single injections are combined in the evaluation where all binding curves are fitted simultaneously. The figure shows an overlay plot of four binding curves and fitted data. The three curves to the left represent sensorgrams with single injections of analyte at 51200 nM but with varying injection times, 10 s, 30 s and 500 s, whereas the curve to the right represents sequential injections of analyte from 800 to 12800 nM. This illustrates that sensorgrams with varying numbers of injections and injection times can be analysed.

It is to be understood that the invention is not limited to the particular embodiments of the invention described above, but the scope of the invention will be established by the appended claims.

CLAIMS

1.　A method of determining kinetic parameters for a reversible molecular interaction between a ligand immobilised to a solid support surface and a binding partner to the ligand in solution, comprising the steps of:

a) sequentially, without intermediate regeneration or renewal of the immobilised ligand, flowing a plurality of fluid volumes containing different known concentrations of the binding partner over the solid support surface to permit association of binding partner to the immobilised ligand,

b) flowing over the solid support surface a fluid volume free from binding partner to permit dissociation of binding partner from the ligand,

c) monitoring during steps a) and b) the momentary amount of binding partner bound to the solid support surface related to time and solution concentration of binding partner and collecting the binding data, and

d) determining the kinetic parameters by globally fitting a predetermined kinetic model for the interaction between the binding partner and the immobilised ligand to the collected binding data, which model allows for mass transport limitation at the solid support surface.

2.　The method according to claim 1, wherein steps a) to c) are repeated at least once with the same or another sequence of binding partner concentrations, and all the collected binding data are fitted simultaneously to the kinetic model in step d).

3.　The method according to claim 1 or 2, wherein sequential binding data obtained from steps a) to c) in claim 1 are combined with at least one set of binding data for a single concentration of binding partner, and the combined binding data are fitted in step d) to the kinetic model.

4.　The method according to claim 1, 2 or 3, wherein step b) in claim 1 is performed after flowing the last fluid volume containing binding partner over the surface.

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5.   The method according to any one of claims 1 to 4, wherein step b) in claim 1 is performed between two fluid volumes containing binding partner.

6.   The method according to claim 4 or 5, wherein each volume containing binding partner is followed by a fluid volume free from binding partner.

7.   The method according to claim 6, wherein one of the fluid volumes free from binding partner, preferably the last fluid volume, is flowed over the solid support surface for a substantially longer time than the other fluid volumes free from binding partner.

8.   The method according to any one of claims 1 to 7, wherein the plurality of fluid volumes containing binding partner include fluid volumes with the same concentration of binding partner.

9.   The method according to any one of claims 1 to 7, wherein the fluid volumes containing binding partner contain successively increasing concentrations of binding partner.

10.   The method according to any one of claims 1 to 9, wherein step a) in claim 1 is stopped when an increased concentration of binding partner results in a predetermined marginal increase in the amount of bound binding partner at the sensor surface.

11.   The method according to any one of claims 1 to 10, wherein the kinetic model is a two-compartment model.

12.   The method according to any one of claims 1 to 11, wherein the kinetic model is adapted to an interaction mechanism selected from 1:1 binding,

parallel reactions, competing reactions, conformation change and bivalent analyte.

13.   The method according to any one of claims 1 to 12, wherein step a) in claim 1 is performed at at least one other density of ligand at the solid support surface.

14.   The method according to any one of claims 1 to 13, wherein the flow over the solid support surface is maintained essentially constant.

15.   A method of determining the concentrations of binding agent in a plurality of samples, wherein the binding agent is capable of interacting with a ligand immobilised to a solid support surface, comprising the steps of:

a) sequentially, without intermediate regeneration or renewal of the immobilised ligand, flowing a plurality of different sample volumes containing binding agent over the solid support surface, ·

. b) flowing over the solid support surface having binding agent bound thereto a fluid volume free from binding agent to permit dissociation of binding --agent from the ligand,

c) monitoring during steps a) and b) the momentary amount of binding agent bound to the solid support surface related to time and solution concentration of binding agent and collecting the binding data, and

d) determining the concentrations of binding agent in the different sample volumes by globally fitting a predetermined kinetic model for the interaction between the binding agent and the immobilised ligand to the collected binding data, which model allows for mass transport limitation at the solid support surface, and wherein the mass transport coefficient is known and kept constant.

16.   The method according to claim 15, wherein also kinetic parameters are determined.
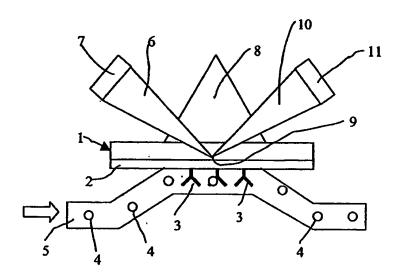
17. A method of determining kinetic parameters for reversible molecular interactions between a ligand immobilised to a solid support surface and a plurality of different binding partners to the ligand in solution, comprising the steps of:

a) sequentially, without intermediate regeneration or renewal of the immobilised ligand, flowing a plurality of fluid volumes containing different binding partners over the solid support surface to permit association of binding partners to the immobilised ligand,

b) after the addition of each fluid volume containing binding partner, flowing over the solid support surface a fluid volume free from binding partner to permit dissociation of binding partner from the ligand,

c) monitoring during steps a) and b) the momentary amount of binding partner bound to the solid support surface related to time and solution concentration of binding partner and collecting the binding data, and

d) determining the kinetic parameters by globally fitting a predetermined kinetic model for the interaction between each binding partner and the immobilised ligand to the collected binding data, which model allows for mass transport limitation at the solid support surface.

18. The method according to any one of claims 1 to 17, wherein the solid support surface is a sensor surface.

19. The method according to any one of claims 1 to 18, wherein the detection at the solid support surface is based on evanescent wave sensing, preferably surface plasmon resonance (SPR).

20. The method according to any one of claims 1 to 19, wherein the detection at the solid support surface is based on detection of a label.

21. The method according to any one of claims 1 to 20, wherein step d) in claims 1, 15 and 17 is computer-implemented.

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22. The method according to any one of claims 1 to 16, wherein steps a) to d) in claims 1, 15 and 17 are computer-implemented.

23. An analytical system for detecting molecular binding interactions, comprising:

(i) a sensor device comprising at least one sensor surface, detection means for detecting molecular interactions at the at least one sensor surface, and means for producing detection data representing the progress of the interactions with time, and

(ii) data processing means for performing the steps as defined in any one of claims 1 to 20.

24. A computer program comprising program code means for performing the method of any one of claims 1 to 20 when the program is run on a computer.

25. A computer program product comprising program code means stored on a computer readable medium or carried on an electrical or optical signal for performing the method of any one of claims 1 to 20 when the program is run on a computer.

26. A computer system containing a program for performing the method of any one of claims 1 to 20.

27 Use of the computer program according to claim 24 or the computer program product according to claim 25 for simulating theoretical interaction data.

ABSTRACT

A method of determining kinetic parameters for a reversible molecular interaction between a ligand immobilised to a solid support surface and a binding partner to the ligand in solution, comprises sequentially, without intermediate regeneration or renewal of the immobilised ligand, flowing a plurality of fluid volumes containing different known concentrations of the binding partner over the solid support surface, monitoring the momentary amount of binding partner bound to the solid support surface related to time and solution concentration of binding partner and collecting the binding data, and determining the kinetic parameters by globally fitting a predetermined kinetic model for the interaction between the binding partner and the immobilised ligand to the collected binding data, which model allows for mass transport limitation at the solid support surface. An analytical system for carrying out the method, a computer program, a computer program product and a computer system for performing the method are also disclosed.

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PRIOR ART

FIG. 1

PRIOR ART

FIG. 2

FIG. 3

FIG. 4

FIG. 5

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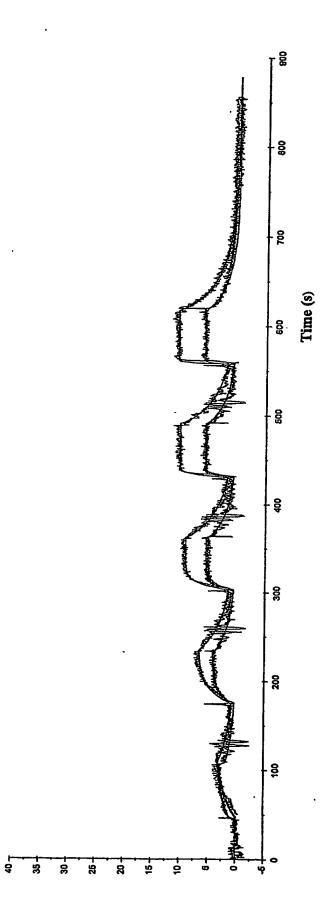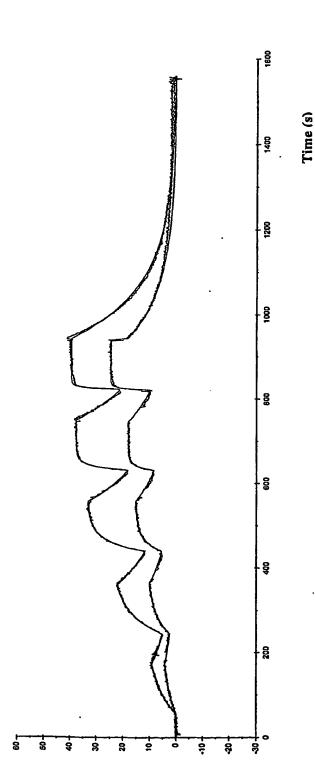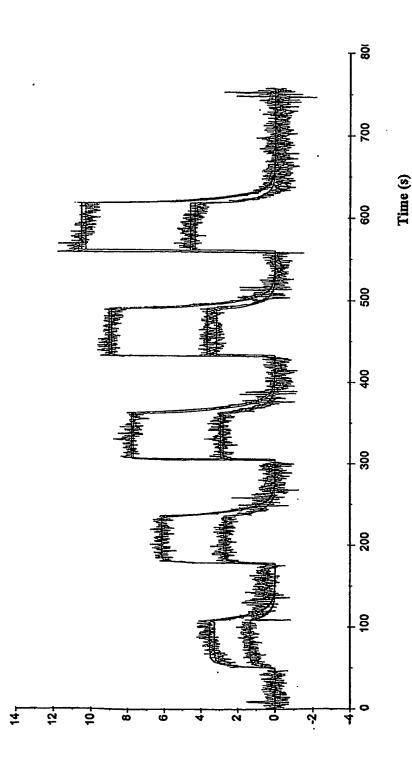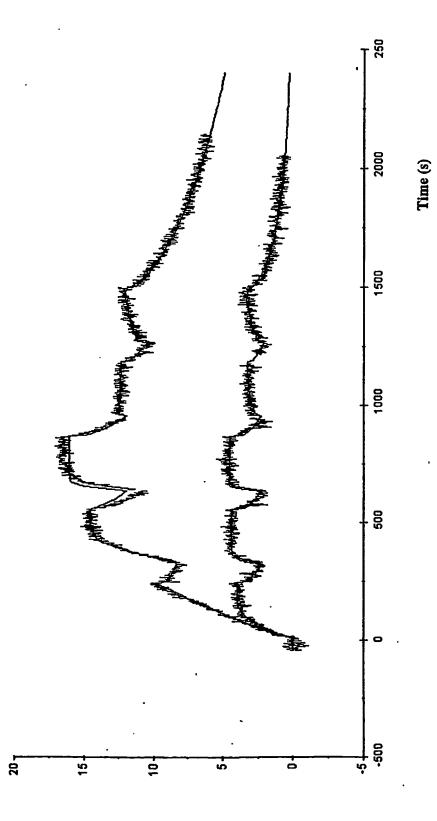Inventor: Robert Karlsson   Serial No.   Docket No.: 740073.469P1

FIG. 6

FIG. 7

FIG. 8

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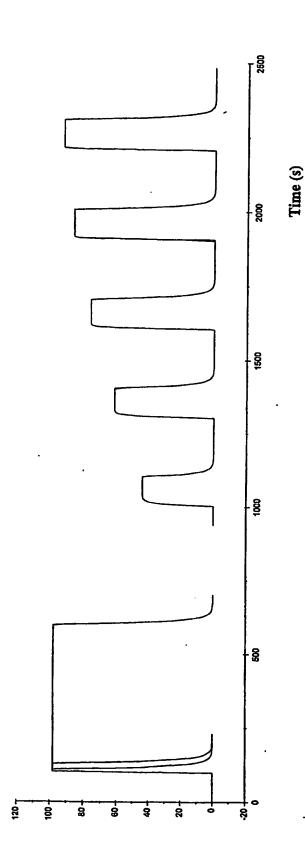Inventor: Robert Karlsson··· ·Serial No.   Docket No.: 740073.469P1

Time (s)

FIG. 9